

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:08:56 ; Search time 299.73 seconds  
(without alignments)  
17.597 Million cell updates/sec

Title: US-09-331-631a-1\_COPY\_29\_73  
Perfect score: 252  
Sequence: 1 SEPDROEYECCKRCQMOLFT.....RCVSQCDKRFREEDIDMSKYD 45

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPTRMBL\_15:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_phase:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	252	100.0	666	10	Q9SP15 macadamia 1
2	252	100.0	666	10	Q9SP14 macadamia 1
3	180	71.4	625	10	Q9SP13 macadamia 1
4	70.5	28.0	525	10	Q43358 theobroma c
5	70.5	28.0	593	10	Q9SEW4 juglans reg
6	67	26.6	810	10	Q9ZW13 cucurbita m
7	67	26.6	1170	6	Q28179 bos taurus
8	65	25.8	393	10	Q9ZTP0 oryza sativ
9	64	25.4	554	10	Q9SG14 arabidopsis
10	63	25.0	564	6	Q9TTS4 gottsch bos taurus
11	62.5	24.8	489	10	Q9SP11 oryza sativ
12	62	24.6	875	4	Q60278 homo sapien
13	62	24.6	941	4	Q9UKT2 homo sapien
14	62	24.6	941	4	Q9UHF8 homo sapien
15	62	24.6	941	4	Q9NZ08 homo sapien
16	62	24.6	1947	2	Q9RFK7 stigmateella
17	61	24.2	554	10	P93719 petunia hyb
18	61	24.2	930	11	Q9J123 ratius norv
19	59.5	23.6	92	5	Q9VTN3 gvtln3 drosophila

20	59.5	23.6	3078	5	Q26031 plasmodium
21	59.5	23.6	3696	5	Q9N4B9 caenorhabdi
22	59	23.4	387	10	Q9S901 arabidopsis
23	58	23.0	242	5	019919 caenorhabdi
24	58	23.0	489	5	061650 drosophila
25	58	23.0	490	5	Q9VFN5 drosophila
26	58	23.0	1421	10	Q49539 arabidopsis
27	57.5	22.8	364	10	Q9LIR8 arabidopsis
28	57	22.6	316	5	Q96288 plasmodium
29	57	22.6	725	12	Q9JF74 vaccinia vl
30	55.5	22.0	205	5	Q9VTA7 drosophila
31	55	21.8	348	5	Q96290 plasmodium
32	55	21.8	402	10	Q9ZRH8 oryza sativ
33	55	21.8	623	10	Q9SU72 arabidopsis
34	55	21.8	822	5	000901 leishmania
35	55	21.8	4123	4	Q75851 homo sapien
36	54.5	21.6	381	5	Q9VTP5 drosophila
37	54.5	21.6	1259	5	Q44971 caenorhabdi
38	54.5	21.6	2703	5	Q9VEG7 drosophila
39	54.5	21.6	2715	5	061603 drosophila
40	54	21.4	314	10	Q40489 arabidopsis
41	54	21.4	607	10	Q9MA04 nicotiana t
42	54	21.4	880	1	Q9U2C8 pyrococcus
43	53.5	21.2	67	5	Q18132 caenorhabdi
44	53.5	21.2	450	4	075595 homo sapien
45	53.5	21.2	450	4	Q9UNA8 homo sapien

## ALIGNMENTS

RESULT 1					
Q9SP15	PRELIMINARY;	PRT;	666 AA.		
ID Q9SP15					
AC Q9SP15					
DT 01-MAY-2000 (TREMBLrel. 13, Created)					
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)					
DE VICILIN PRECURSOR.					
GN AMP2.					
OS Macadamia integrifolia (Macadamia nut).					
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;					
OC Magnoliophyta; Eudicotyledons; Proteaceae; Macadamia.					
OX NCBI_TaxID=60698;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=NUT KERNEL;					
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;					
RT "A family of antimicrobial peptides is produced by processing of a 7S					
RT globulin protein in Macadamia integrifolia kernels.";					
RL Plant J. 0:0-0(1999).					
DR EMBL; AF161883; AAD54244.1; -					
DR HSSP; P02853; 2PHL.					
DR INTERPRO; IPR001113; -					
DR PFM; PF00546; Seedstore_7s; 1.					
DR SEQUENCE 666 AA; 78217 MW; C752B884B2DF0224 CRC64;					
Query Match	100.0%;	Score 252;	DB 10;	Length 666;	
Best Local Similarity	100.0%;	Pred. No. 5;	9e-24;		
Matches 45;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
OY 1 SEPDROEYECCKRCQMOLFTSGMRCVSQCDKRFREEDIDMSKYD 45					
Db 29 SEPDROEYECCKRCQMOLFTSGMRCVSQCDKRFREEDIDMSKYD 73					
RESULT 2					
ID Q9SP14	PRELIMINARY;	PRT;	666 AA.		
AC Q9SP14					
DT 01-MAY-2000 (TREMBLrel. 13, Created)					
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)					

DT 01-OCT-2000 (Tremblrel. 15, last annotation update)  
DE VICILIN PRECURSOR.  
GN AMP2.  
OS Macadamia integrifolia (Macadamia nut).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.  
OX NCBI\_TaxID=60698;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=NOT KERNEL;  
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;  
RT "A family of antimicrobial peptides is produced by processing of a 7S  
globulin protein in Macadamia integrifolia.";  
RL Plant J. 0:0-0(1999).  
DR EMBL; AF161884; AAD54245.1; -.  
DR HSSP; P02853; 2PHL.  
DR INTERPRO: IPR001113; -.  
DR PFAM: PF00546; Seedstore\_7s; 1.  
SQ SEQUENCE 666 AA; 78243 MW; 0ECA22E8710F8A7B CRC64;

Query Match 100.0%; Score 252; DB 10; Length 666;  
Best Local Similarity 100.0%; Pred. No. 5.9e-24;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEPDROEYECCKROCMOLETSGOMRRCVSOCCKRFEEDIDMSKYD 45  
DB 29 SEPDROEYECCKROCMOLETSGOMRRCVSOCCKRFEEDIDMSKYD 73

RESULT 3  
O9SPL3 ID O9SPL3 PRELIMINARY; PRT; 625 AA.  
AC O9SPL3;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)  
DT 01-OCT-2000 (Tremblrel. 15, last annotation update)  
DE VICILIN PRECURSOR (FRAGMENT).  
GN AMP2.  
OS Macadamia integrifolia (Macadamia nut).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.  
OX NCBI\_TaxID=60698;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=NOT KERNEL;  
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;  
RT "A family of antimicrobial peptides is produced by processing of a 7S  
globulin protein in Macadamia integrifolia.";  
RL Plant J. 0:0-0(1999).  
DR EMBL; AF161885; AAD54246.1; -.  
DR HSSP; P02853; 2PHL.  
DR INTERPRO: IPR001113; -.  
DR PFAM: PF00546; Seedstore\_7s; 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 625 AA; 73586 MW; 415808A89D370296 CRC64;

Query Match 71.4%; Score 180; DB 10; Length 625;  
Best Local Similarity 100.0%; Pred. No. 6.8e-15;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 QCMOLETSGOMRRCVSOCCKRFEEDIDMSKYD 45  
DB 1 QCMOLETSGOMRRCVSOCCKRFEEDIDMSKYD 32

RESULT 4  
O43358 ID O43358 PRELIMINARY; PRT; 525 AA.  
AC O43358;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)

DT 01-OCT-2000 (Tremblrel. 15, last annotation update)  
DE VICILIN PRECURSOR.  
GN CSV.  
OS Theobroma cacao (Cacao).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II;  
OC Malvales; Malvaceae; Theobroma.  
OX NCBI\_TaxID=3641;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LEAVES;  
RX MEDLINE=92286309; PubMed=1600151;  
RA Moehentz L., Fritz P.J.;  
RT "Comparison of the structure and nucleotide sequences of vicilin genes  
of cocoa and cotton raise questions about vicilin evolution.";  
RL Plant Mol. Biol. 18:1173-1176(1992).  
DR EMBL; X62625; CAA44493.1; -.  
DR EMBL; X62626; CAA44494.1; -.  
DR HSSP; P02853; 2PHL.  
DR MENDEL; 30919; Thecc:1188;30919.  
DR INTERPRO: IPR001113; -.  
DR PFAM: PF00546; Seedstore\_7s; 1.  
DR PRODOM; PD081059; -. 1.  
KW Signal.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 525 VICILIN.  
SQ SEQUENCE 525 AA; 60798 MW; 19114CD5C248905D CRC64;

Query Match 28.0%; Score 70.5; DB 10; Length 525;  
Best Local Similarity 32.4%; Pred. No. 0.39;  
Matches 11; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

OY 5 ROEYECCKROCMOLET-SGOMRRCVSOCCKRFEED 37  
DB 39 ROEYECCKROCMOLET-SGOMRRCVSOCCKRFEED 72

RESULT 5  
O9SEW4 ID O9SEW4 PRELIMINARY; PRT; 593 AA.  
AC O9SEW4;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)  
DT 01-OCT-2000 (Tremblrel. 15, last annotation update)  
DE VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).  
OC Juglans regia (English walnut).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I;  
OX NCBI\_TaxID=51240;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. SUNLAND; TISSUE=SOMATIC EMBRYO LINE;  
RA Teuber S.S., Jarvis K.C., Peterson W.R., Danekar A.M., Ansari A.A.;  
RT "Identification and cloning of a cDNA encoding a vicilin-like protein,  
Jug r 2, from English walnut kernel (Juglans regia): a major food  
allergen.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF066053; AAF18269.1; -.  
DR HSSP; P02853; 2PHL.  
DR INTERPRO: IPR001113; -.  
DR PFAM: PF00546; Seedstore\_7s; 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 593 AA; 69990 MW; 9BA127E19B18C0D8 CRC64;

Query Match 28.0%; Score 70.5; DB 10; Length 593;  
Best Local Similarity 29.4%; Pred. No. 0.44;  
Matches 10; Conservative 15; Mismatches 8; Indels 1; Gaps 1;  
OY 5 ROEYECCKROCMOLETSGOMRRCVSOCCKRFEED 37  
DB 11 ROEYECCKROCMOLETSGOMRRCVSOCCKRFEED 72

Db 120 Q00YHRCRCRCQIOE0SPEROROCQRCEROYKE 153

RESULT 6

ID 092WT13 PRELIMINARY; PRT; 810 AA.

AC 092WT13;

DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE pvi100.

OS Cucurbita maxima (Pumpkin) (Winter squash).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;

OC Cucurbitales; Cucurbitaceae; Cucurbita.

OX NCBI\_Taxid=3661;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=KUKOKAWA AMAKURI NANKIN; TISSUE=COTYLEDON;

RX MEDLINE=99107919; PubMed=9891029;

RA Yamada K., Shimada T., Kondo M., Nishimura M., Hara-Nishimura I.;

RT "Multiple functional proteins are produced by cleaving Asn-Gln bonds

RT of a single precursor by vacuolar processing enzyme.";

RL J. Biol. Chem. 274:2563-2570(1999).

DR EMBL; AB019195; BAA34056.1; -.

DR HSSP; P02853; 2PHL.

DR INTERPRO; IPR001113; -.

DR PFAM; PF00546; Seedstore\_7s; 1.

DR PRODOM; PD081059; -; 1

SO SEQUENCE 810 AA; 97314 MW; A829A3F7542266AB CRC64;

Query Match 26.6%; Score 67; DB 10; Length 810;

Best Local Similarity 34.1%; Pred. No. 1.6;

Matches 15; Conservative 6; Mismatches 15; Indels 8; Gaps 2;

OY 5 ROYEBCRCQCMLETS-GQMRRCVSQCKRFE-----EDID 40

Db 75 RAEEVCHRLRCQVAREGVEQQRCKEQVCEERLREREGRGEDVD 118

RESULT 7

ID 028179 PRELIMINARY; PRT; 1170 AA.

AC 028179;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE THROMBOSPONDIN 1.

GN TSP-1.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI\_Taxid=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HOLSTEIN; TISSUE=ANTERIOR TOOTH;

RX MEDLINE=98173773; PubMed=9507054;

RA Ueno A., Yamashita K., Nagata T., Tsurumi C., Miwa Y., Kitamura S.,

RA Inoue H.;

RT "cDNA cloning of bovine thrombospondin 1 and its expression in

RT odontoblasts and predentin.";

RL Blochim. Biophys. Acta 1382:17-22(1998).

RN [2]

RP SEQUENCE OF 1-18 FROM N.A.

RC TISSUE=AORTIC ENDOTHELIUM;

RA Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;

RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; X87619; CAA60951.1; -.

DR HSSP; P35555; 1BMN.

DR INTERPRO; IPR000561; -.

DR INTERPRO; IPR00084; -.

DR INTERPRO; IPR001007; -.

DR INTERPRO; IPR001791; -.

DR INTERPRO; IPR001881; -.

DR INTERPRO; IPR002465; -.

DR INTERPRO; IPR003129; -.

DR PFAM; PF00008; EGF; 2.

DR PFAM; PF00090; TSP\_1; 3.

DR PFAM; PF00093; WVC; 1.

DR PFAM; PF02210; TSPN; 1.

DR PROSITE; PS00340; RECEPTOR\_CYTOKINES\_2; UNKNOWN\_2.

DR PROSITE; PS01186; EGF\_2; 1.

DR PROSITE; PS01208; WVC; 1.

SO SEQUENCE 1170 AA; 129533 MW; 0DD6ADF3E5FA031A CRC64;

Query Match 26.6%; Score 67; DB 6; Length 1170;

Best Local Similarity 39.5%; Pred. No. 2.3;

Matches 15; Conservative 6; Mismatches 11; Indels 6; Gaps 2;

OY 13 ROCMQLE-----TSQMRRC-VSQCCKRFEEDIDMSKY 44

Db 404 RSCDSLNNRCBSSVQTRTCHIQCDKRFKODGGMSHW 441

RESULT 8

ID 092TP0 PRELIMINARY; PRT; 393 AA.

AC 092TP0;

DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)

DE HYPOTHETICAL 45.3 KDA PROTEIN.

GN OSE705.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

OX NCBI\_Taxid=4530;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=LONMELLO;

RA Chen P.W., Chen L.J.;

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF049348; AAD02494.1; -.

KM Hypothetical protein.

SO SEQUENCE 393 AA; 45258 MW; DBD01934BA2F9E95 CRC64;

Query Match 25.8%; Score 65; DB 10; Length 393;

Best Local Similarity 36.8%; Pred. No. 1.5;

Matches 14; Conservative 7; Mismatches 15; Indels 2; Gaps 1;

OY 5 ROYEBCRCQCM-QLETSQMRRCVSQCKRFEEDID 40

Db 37 KEELRWCKKOCRWEGADODRLRCEBCQCLQROGEDDD 74

RESULT 9

ID 09SG14 PRELIMINARY; PRT; 554 AA.

AC 09SG14;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE PUTATIVE GTPASE ACTIVATOR PROTEIN OF RAB-LIKE SMALL GTPASES (GTPASE

DE ACTIVATING-LIKE PROTEIN).

GN TG12.5 OR P2K15.210.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

OC Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_Taxid=3702;

RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-CV, COLUMBIA;  
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,  
 RA Ranning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,  
 RA Bowman C.L., White O., Niernan W.C., Fraser C.M.;  
 RT "Arabidopsis thaliana chromosome I BAC TIC12 genomic sequence."  
 RN Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RL [1]  
 RP SEQUENCE FROM N.A.  
 RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,  
 RA Mewes H.W., Lemcke K., Mayer K.F.X., Queiler F., Salanoubat M.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL EMBL: AC012329; AAF16581.1; -;  
 DR EMBL: AL132956; CAB66414.1; -;  
 DR INTERPRO: IPR00195; -;  
 DR PFAM: PF00566; TBC; 1;  
 SQ SEQUENCE 554 AA; 63583 MW; 430BE1FCF1D8901C CRC64;

Query Match 25.4%; Score 64; DB 10; Length 554;  
 Best Local Similarity 28.2%; Pred. No. 2.7;  
 Matches 11; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 5 ROEYEECKRQCMOLETSGQMRRCVSCQCKRFEEDIDMSK 43  
 DB 148 RKEVERLRROCKRLQKHNNGTRKLYNGSETIQDEYDMPR 186

RESULT 10  
 Q9TTS4  
 ID 09TTS4 PRELIMINARY; PRT; 564 AA.  
 AC 09TTS4;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (T-EMBLrel. 14, Last annotation update)  
 DE SCO-SPONDIN (FRAGMENT).  
 GN SCO-SPONDIN.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-SUBCOMMISSURAL ORGAN.  
 RA Gobdon S., Creveaux I., Monnerie H., El Bitar F., Didier R.,  
 RA Herbet A., Melniet R., Bamdad M., Dastugue B., Melniet A.;  
 RT "Characterization of cattle SCO-spondin glycoprotein."  
 RN Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: A1312107; CAB53760.1; -;  
 DR INTERPRO: IPR001846; -;  
 DR INTERPRO: IPR002919; -;  
 DR PFAM: PF00094; vwd; 1.  
 DR PFAM: PF01826; TIL; 2.  
 FT NON\_TER 1 564  
 FT NON\_TER 1 564  
 SQ SEQUENCE 564 AA; 60337 MW; 2E22DA242F9BBE7C CRC64;

Query Match 25.0%; Score 63; DB 6; Length 564;  
 Best Local Similarity 38.7%; Pred. No. 3.7;  
 Matches 12; Conservative 6; Mismatches 9; Indels 4; Gaps 1;

QY 6 QEYEE-----CKRQCMOLETSGQMRRCVSCQCD 32  
 DB 480 QEYECAPACDRNGCEPDEGELDNCVACGN 510

RESULT 11

Q9SP11  
 ID Q9SP11 PRELIMINARY; PRT; 489 AA.  
 AC Q9SP11;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)  
 DE SUCROSE BINDING PROTEIN HOMOLOG S-64.  
 GN SBP.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;  
 OC Fabales; Fabaceae; Papilionoideae; Glycine.  
 OX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pedra J.H.F., Delu-Flho N., Pirovani C.P., Contim L.S., Dewey R.E.,  
 RA Oroni W.C., Fontes E.P.B.;  
 RT "Antisense and sense expression of a sucrose binding protein homologue  
 RT gene from soybean in transgenic tobacco affects plant growth and  
 RT carbohydrate partitioning in leaves."  
 RL Plant Sci. 0:0-0(1999).  
 DR EMBL: AF191299; AAF05723.1; -;  
 DR HSSP: P02853; 2PHL.  
 DR INTERPRO: IPR001113; -;  
 DR PFAM: PF00546; Seedstore\_7s; 1.  
 SQ SEQUENCE 489 AA; 55834 MW; 9BBC0D45EDCECD2 CRC64;

Query Match 24.8%; Score 62.5; DB 10; Length 489;  
 Best Local Similarity 36.6%; Pred. No. 3.7;  
 Matches 15; Conservative 3; Mismatches 14; Indels 9; Gaps 2;

QY 7 EYECKRQCMOLE--TSGQMRRCVSCQD-----KRFED 38  
 DB 38 EIVTCKHQCGQGRQYTESDKRTLQCGDSMKQREKQVEEE 78

RESULT 12  
 ID 060278 PRELIMINARY; PRT; 875 AA.  
 AC 060278;  
 DT 01-AUG-1998 (T-EMBLrel. 07, Created)  
 DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)  
 DT 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)  
 DE KIAA0525 PROTEIN (FRAGMENT).  
 GN KIAA0525.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN.  
 RX MEDLINE=98280545; PubMed=9628581;  
 RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,  
 RA Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. IX.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro."  
 RL DNA Res. 5:31-39(1998).  
 DR EMBL: AB011097; BAA25451.1; -;  
 DR MEROPS: M01.018; -;  
 DR INTERPRO: IPR00130; -;  
 DR INTERPRO: IPR001930; -;  
 DR PFAM: PF01433; Peptidase\_M1; 1.  
 DR PRINTS: PR00756; ALADIPTASE.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 FT NON\_TER 1 875  
 FT NON\_TER 1 875  
 SQ SEQUENCE 875 AA; 99522 MW; C31A77DE516DEAFE CRC64;

Query Match 24.6%; Score 62; DB 4; Length 875;  
 Best Local Similarity 37.8%; Pred. No. 7.6;

Matches 14: Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 5 ROYEBCRQCMOLETSGOMRCVSCDCKRFEEDIDW 41  
| | | | | : | | | | | : | | | |  
Db 812 RTRLEEVKGFSSLKENGSQLRCVQOTITEENIGW 848

## RESULT 13

Q9UKY2 PRELIMINARY; PRT; 941 AA.  
AC Q9UKY2;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE AIPOCYTE-DERIVED LEUCINE AMINOPEPTIDASE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9238715; Pubmed=10220586;  
RA Hattori A., Matsumoto H., Mizutani S., Tsujimoto M.;  
RT "Molecular cloning of adipocyte-derived leucine aminopeptidase highly  
related to placental leucine aminopeptidase/oxytocinase.";  
RL J. Biochem. 125:931-938(1999).  
DR EMBL: AF106037; AAF07395.1; -.  
DR INTERPRO: IPR000130; -.  
DR INTERPRO: IPR001930; -.  
DR PFAM: PF01433; Peptidase\_M1.1.  
DR PRINTS: PR00756; ALADIPASE.  
DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Aminopeptidase.  
SQ SEQUENCE 941 AA; 107187 MW; 46BEP7CF78DEBC1 CRC64;

Query Match 24.6%; Score 62; DB 4; Length 941;  
Best Local Similarity 37.8%; Pred. No. 8.1;  
Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 5 ROYEBCRQCMOLETSGOMRCVSCDCKRFEEDIDW 41  
| | | | | : | | | | | : | | | |  
Db 885 RTRLEEVKGFSSLKENGSQLRCVQOTITEENIGW 921

## RESULT 14

Q9UHF8 PRELIMINARY; PRT; 941 AA.  
AC Q9UHF8;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE AMINOPEPTIDASE PILS.  
GN APPILS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Schomburg T.;  
RT "Molecular characterization of human aminopeptidase PILS.";  
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF183569; AAF20384.1; -.  
DR INTERPRO: IPR000130; -.  
DR INTERPRO: IPR001930; -.  
DR PFAM: PF01433; Peptidase\_M1.1.  
DR PRINTS: PR00756; ALADIPASE.  
DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Aminopeptidase.  
SQ SEQUENCE 941 AA; 107420 MW; 2ECA71F0BACBFD74 CRC64;

Query Match 24.6%; Score 62; DB 4; Length 941;  
Best Local Similarity 37.8%; Pred. No. 8.1;  
Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 5 ROYEBCRQCMOLETSGOMRCVSCDCKRFEEDIDW 41  
| | | | | : | | | | | : | | | |  
Db 885 RTRLEEVKGFSSLKENGSQLRCVQOTITEENIGW 921

## RESULT 15

Q9NZ08 PRELIMINARY; PRT; 941 AA.  
AC Q9NZ08;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE TYPE 1 TUMOR NECROSIS FACTOR RECEPTOR SHEDDING AMINOPEPTIDASE  
REGULATOR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Cui X., Alsady S., Lawrence M., Combs C.A., Roulhani F.N.,  
RA Levine S.J.;  
RT "Identification of an Aminopeptidase Regulator of Type I Tumor  
Necrosis Factor Receptor Shedding.";  
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF222340; AAF34664.1; -.  
DR RECEPTOR: Aminopeptidase.  
KW Receptor.  
SQ SEQUENCE 941 AA; 107234 MW; 22A0795C90155F04 CRC64;

Query Match 24.6%; Score 62; DB 4; Length 941;  
Best Local Similarity 37.8%; Pred. No. 8.1;  
Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 5 ROYEBCRQCMOLETSGOMRCVSCDCKRFEEDIDW 41  
| | | | | : | | | | | : | | | |  
Db 885 RTRLEEVKGFSSLKENGSQLRCVQOTITEENIGW 921

Search completed: March 1, 2001, 16:08:59  
Job time: 1543 sec

